

Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) An isolated *rpoB* gene or gene fragment of a bacterium of the genus *Streptococcus* and 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, comprising a nucleic acid sequence selected from the group consisting of:

a. SEQ ID Nos:8-10, 13, 15-21, and 24-35 in which:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T, and

N nucleotide represents A, T, C, G or I;

b. the full-length complementary sequences of the nucleic acid sequences of

(a); and

c. sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b).

2. (Currently Amended) An isolated *rpoB* gene of claim 1 wherein the bacterium is one of the bacteria *Streptococcus anginosus*, *Streptococcus equinus*, *Abiotrophia defectiva* and *Enterococcus faecalis*, comprising a nucleic acid sequence selected from the group consisting of:

a. SEQ ID NOs:1-3 and SEQ ID NO:5 wherein:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T, and

N nucleotide represents A, T, C, G or I, and I;

b. the full-length complementary sequences of the nucleic acid sequences of

(a); and

c. sequences having at least 98.7% homology to the nucleic acid sequences of

(a) or (b).

3. (Currently Amended) An isolated *rpoB* gene fragment of a bacterium of the genus *Streptococcus* and of 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, comprising a nucleic acid sequence selected from the group consisting of:

(a) SEQ ID NOs:8-35, in which:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T, and

N nucleotide represents A, T, C or G; and

(b) the full-length complementary sequences of the nucleic acid sequences of

(a), and (a); and

(c) sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b).

4. (Currently Amended) An isolated oligonucleotide, comprising:

(a) a nucleic acid sequence specific to a bacterium of genus *Streptococcus* and 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, and comprising 20-100 consecutive nucleotides included in one of nucleic acid sequences SEQ ID NOs:8-35, in which:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T, and

N nucleotide represents A, T, C or G;

(b) the full-length complementary sequences of the nucleic acid sequences of (a); and

(c) sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b).

5-6. (Canceled)

7. (Currently Amended) A mixture of oligonucleotides, consisting of comprising:

an equimolar mixture of oligonucleotides ~~as defined in claim 6~~, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and is at least 12 nucleotides in length and comprises at least 8 consecutive nucleotides of the full-length sequence set forth in SEQ ID NO:6 or SEQ ID NO:7, or at least 8 consecutive nucleotides of the full-length complementary sequences thereof, where:

N represents, for the equimolar mixture, inosine or N represents, for the equimolar mixture, equimolar amounts of A, T, C, and G,

R represents A or G,

M represents A or C, and

Y represents C or T.

~~said sequence included in SEQ ID NO:6 or sequence included in SEQ ID NO:7 or complementary sequence thereof.~~

8. (Currently Amended) A mixture of oligonucleotides according to claim 7, comprising wherein the an equimolar mixture of oligonucleotides comprises of 32 said different oligonucleotides as defined in claim 6, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and comprises at least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:6, or at least 15 consecutive nucleotides of the full-length complementary sequence thereof, where: included in the following sequence:

~~SEQ ID NO:6 5' AARYTNGGMCCCTGAAGAAAT 3'~~

~~in which:~~

R represents A or G,

Y represents C or T,

M represents A or C, and

N represents A, T, C or G,

~~or in a complementary sequence thereof.~~

9. (Currently Amended) A mixture of oligonucleotides according to claim 7, consisting of wherein the an equimolar mixture of oligonucleotides comprises of 8 said different oligonucleotides as defined in claim 6, wherein each oligonucleotide in the

equimolar mixture of oligonucleotides has a different sequence and comprises at least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:6, or at least 15 consecutive nucleotides of the full-length complementary sequence thereof, where: included in the following sequence:

~~SEQ ID NO:6 5' AARYTNGGMCCCTGAAGAAAT 3'~~

in which:

R represents A or G,

Y represents C or T,

M represents A or C, and

N represents inosine, inosine.

or in a complementary sequence thereof.

10. (Currently Amended) A mixture of oligonucleotides according to claim 7, consisting of wherein the an equimolar mixture of oligonucleotides comprises 16 said different oligonucleotides as defined in claim 6, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and comprises at least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:7, or at least 15 consecutive nucleotides of the full-length complementary sequence thereof, where: included in the following sequence:

~~SEQ ID NO:7 5' TGNARTTTRTCATCAACCATGTG 3'~~

in which:

R represents A or G, and

N represents A, T, C or G

or in a complementary sequence thereof.

11. (Currently Amended) A mixture of oligonucleotides according to claim 7,
~~consisting of an~~ wherein the equimolar mixture of oligonucleotides comprises 4-said different
oligonucleotides as defined in claim 6, wherein each oligonucleotide in the equimolar mixture
of oligonucleotides has a different sequence and comprises at least 15 consecutive
nucleotides of the sequence set forth in SEQ ID NO:7, or at least 15 consecutive nucleotides
of the full-length complementary sequence thereof, where: included in the following
sequence:

~~SEQ ID NO:7 5' TGNARTTTRTCATCAACCATGTG 3'~~

in which:

R represents A or G, and

N represents inosine,

~~or in a complementary sequence thereof.~~

12. (Currently Amended) A mixture of oligonucleotides according to claim 7,
~~consisting of an equimolar mixture of oligonucleotides as defined in claim 6~~, wherein each
oligonucleotide in the equimolar mixture of oligonucleotides ~~has a different sequence~~
~~consisting of said sequence included in SEQ ID NO:6 or sequence included in SEQ ID NO:7~~
~~or complementary sequence thereof~~ consists of the sequence set forth in SEQ ID NO:6, SEQ
ID NO:7, or the full-length complementary sequences thereof.

13-14. (Canceled)

15. (Withdrawn-Currently Amended) A method for detecting the presence of a
bacterium of genus *Streptococcus* or of 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia*
and *Granulicatella*, comprising:

[[1-]]1. contacting at least one genus probe comprising a mixture of oligonucleotides as in claim 7, with a ~~specimen~~ sample containing or possibly containing nucleic acids of at least one said bacterium, and

[[2-]]2. determining the formation or non-formation of a ~~hybridisation~~ hybridization complex between said genus probe and nucleic acids of the specimen, wherein the presence of said bacterium in the specimen is indicated by formation of a ~~hybridisation~~ hybridization complex.

16. (Withdrawn-Currently Amended) A method for detecting the presence of a bacterium of genus *Streptococcus* or of 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, comprising:

[[1-]]1. contacting amplification primers comprising mixtures of oligonucleotides as in claim 7, with a ~~specimen~~ sample containing or possibly containing nucleic acids of at least one said bacterium, ~~and with~~ wherein:

~~as 5' primer, a said mixture of oligonucleotides comprising a sequence included in SEQ ID NO:6, or a complementary sequence thereof, and~~

~~as 3' primer a said mixture of oligonucleotides comprising a sequence included in SEQ ID NO:7, or a complementary sequence thereof.~~

a 5' primer comprises an equimolar mixture of oligonucleotides,
wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different
sequence and is at least 12 nucleotides in length and comprises at least 8 consecutive
nucleotides of the sequence set forth in SEQ ID NO:6, or at least 8 consecutive nucleotides of
the full-length complementary sequence thereof, and

a 3' primer comprises an equimolar mixture of oligonucleotides,
wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different

sequence and is at least 12 nucleotides in length and comprises at least 8 consecutive nucleotides of the sequence set forth in SEQ ID NO:7, or at least 8 consecutive nucleotides of the full-length complementary sequence thereof; and

[[2-]]2. amplifying nucleic acids by enzymatic polymerisation-polymerization reaction to determine the presence or absence of an amplification product, wherein occurrence of an amplification product indicates the presence of said bacterium in the specimen sample.

17. (Canceled)

18. (Withdrawn-Currently Amended) A method for detecting whether a given species of a bacterium of genus *Streptococcus* or related genera is present in a sample, said given species of a bacterium selected from the group of species consisting of:

Streptococcus mutans, Streptococcus oralis, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus salivarius, Streptococcus sanguinis, Streptococcus suis, Streptococcus acidominimus, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus constellatus, Streptococcus difficile, Streptococcus dysgalactiae, Streptococcus equi, Streptococcus equinus, Streptococcus intermedius, Streptococcus mitis, Streptococcus bovis, Streptococcus alactolyticus, Streptococcus galloyticus, Streptococcus macedonicus, Streptococcus infantarius, Streptococcus hominis, Granulicatella adjacens, Abiotrophia defectiva, Enterococcus avium, Enterococcus casselliflavus, Enterococcus faecalis, Enterococcus faecium, Enterococcus gallinarum, Enterococcus sphaerolyticus, Gemella haemolysans, and Gemella morbillorum,

~~a method in which, in a specimen containing or possibly containing nucleic acids of at least one said bacterium, the method comprising:~~

a) sequencing an amplified *rpoB* gene fragment of a bacterium using nucleotide primers ~~consisting of comprising~~ said oligonucleotide mixtures as in claim 7, comprising sequences included in SEQ ID NO:6 as 5' primer and in SEQ ID NO:7 as 3' primer, or complementary sequences thereof, and wherein:

a 5' primer comprises an equimolar mixture of oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and is at least 12 nucleotides in length and comprises at least 8 consecutive nucleotides of the sequence set forth in SEQ ID NO:6, or at least 8 consecutive nucleotides of the full-length complementary sequence thereof, and

a 3' primer comprises an equimolar mixture of oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and is at least 12 nucleotides in length and comprises at least 8 consecutive nucleotides of the sequence set forth in SEQ ID NO:7, or at least 8 consecutive nucleotides of the full-length complementary sequence thereof; and

b) wherein determining the presence or absence of the given species of said bacterium ~~is determined~~ by comparing the sequence obtained of said fragment with the sequence of the complete *rpoB* gene of said bacterium or the sequence of a *rpoB* gene fragment of said bacterium respectively comprising said sequences SEQ ID NOs:8-35 and the full-length complementary sequences thereof, where:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T, and

N nucleotide represents A, T, C, G or I;

wherein the presence of said bacterium in the ~~specimen~~ sample is determined if the obtained sequence of said fragment is identical to the known sequence of the *rpoB* gene or gene fragment of said bacterium.

19–21. (Cancelled)

22. (Withdrawn-New) The method according to claim 16, further comprising:

3. determining whether at least one species selected from the group consisting of *Streptococcus mutans*, *Streptococcus oralis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus suis*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus difficile*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus equinus*, *Streptococcus intermedius*, *Streptococcus mitis*, *Streptococcus bovis*, *Streptococcus alactolyticus*, *Streptococcus galloyticus*, *Streptococcus macedonicus*, *Streptococcus infantarius*, *Streptococcus hominis*, *Granulicatella adjacens*, *Abiotrophia defectiva*, *Enterococcus avium*, *Enterococcus casselliflavus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus sphaerolyticus*, *Gemella haemolysans*, and *Gemella morbillorum*, is present in the sample by contacting the amplification product with at least one species probe comprising a nucleic acid sequence selected from the group consisting of the sequences set forth in SEQ ID NOs:8-35 and the full-length complementary sequences thereof, where:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T, and

N nucleotide represents A, T, C or G; and

4. determining formation or non-formation of a hybridization complex

between said species probe and the amplification product, wherein the formation of a

hybridization complex indicates the presence of said at least one species in the sample.